CLAIM AMENDMENTS

Claims 1-28 (withdrawn)

29. (currently amended) A method of identifying a compound which modulates the interaction of GRF4 with Ras, comprising

a) contacting (i) GRF4 or a portion of GRF4 selected from the group consisting of a Ras association domain and a CDC25-related GEF domain~~, a Ras-binding fragment of GRF4 or a derivative of either of the foregoing (ii),~~ with (ii) Ras ~~a GRF4-binding fragment of Ras or a derivative of either of the foregoing~~ in the presence of the compound~~; wherein (i) and (ii) are capable of binding~~; and

b) determining whether the binding between (i) and (ii) is modulated compared to a control for determining the binding of GRF4 and Ras in the absence of the compound, ~~thereby~~ wherein an increase or decrease in binding in the presence of the compound indicates ~~indicating~~ that the compound modulates the interaction of GRF4 and Ras.

30. (currently amended)_____ A method of identifying a compound which modulates the interaction of GRF4 with Rap1, comprising

a) contacting (i) GRF4 or a portion of GRF4 selected from the group consisting of a Ras association domain ~~or~~and a CDC25-related GEF domain~~, a Rap1-binding fragment of GRF4 or a derivative of either of the foregoing~~ with (ii) Rap1 ~~, a GRF4-binding fragment of Rap1 or a derivative of either of the foregoing~~ in the presence of the compound; ~~wherein (i) and (ii) are capable of binding; and~~

b) determining whether the binding between (i) and (ii) is modulated compared to a control for determining the binding of GRF4 and Rap1 in the absence of the compound, wherein an increase or decrease in binding in the presence of the compound indicates ~~thereby indicating~~ that the compound modulates the interaction of GRF4 and Rap1.

31. (currently amended) A method of evaluating the cell proliferation reducing properties of a compound comprising contacting the compound with:

a) (I) GRF4, or a portion of GRF4 selected from the group consisting of a Ras association domain or a CDC25-related GEF domain~~a Ras binding fragment of GRF4 or a derivative of either of the foregoing~~; and

b) (ii) Ras,- in the presence of the compound ~~a GRF4 binding fragment of Ras or a derivative of either of the foregoing; wherein (a) and (b) are capable of binding~~; and

c) determining whether the binding between (i) and (ii) is ~~modulated~~ inhibited compared to a control for determining the binding of GRF4 and Ras in the absence of the compound, wherein ~~an increase or decrease~~an inhibition of binding in the presence of the compound indicates~~the ability of the compound to interfere with the binding of a) with b), the ability to interfere with binding indicating~~ that the compound reduces cell proliferation.

Claims 32-35 (withdrawn)

36. (new) The method of claim 29, wherein the GRF4 comprises the following sequence motifs and domains, in amino to carboxyl order: a cyclic nucleotide monophosphate-binding domain, a Ras exchange motif, a PDZ association domain, a Ras association domain, a CDC25-related GEF domain, a first PY motif, a second PY motif, and a COOH-terminal SaV sequence conforming to a PDZ binding motif.

37. (new) The method of claim 29, wherein the GRF4 comprises SEQ ID NO:2 or a sequence of at least 80% sequence identity to SEQ ID NO:2.

38. (new) The method of claim 30, wherein the GRF4 comprises the following sequence motifs and domains, in amino to carboxyl order: a cyclic nucleotide monophosphate-

binding domain, a Ras exchange motif, a PDZ association domain, a Ras association domain, a CDC25-related GEF domain, a first PY motif, a second PY motif, and a COOH-terminal SaV sequence conforming to a PDZ binding motif.

39. (new) The method of claim 30, wherein the GRF4 comprises SEQ ID NO:2 or a sequence of at least 80% sequence identity to SEQ ID NO:2.

40. (new) The method of claim 31, wherein the GRF4 comprises the following sequence motifs and domains, in amino to carboxyl order: a cyclic nucleotide monophosphate-binding domain, a Ras exchange motif, a PDZ association domain, a Ras association domain, a CDC25-related GEF domain, a first PY motif, a second PY motif, and a COOH-terminal SaV sequence conforming to a PDZ binding motif.

41. (new)The method of claim 31, wherein the GRF4 comprises SEQ ID NO:2 or a sequence of at least 80% sequence identity to SEQ ID NO:2.